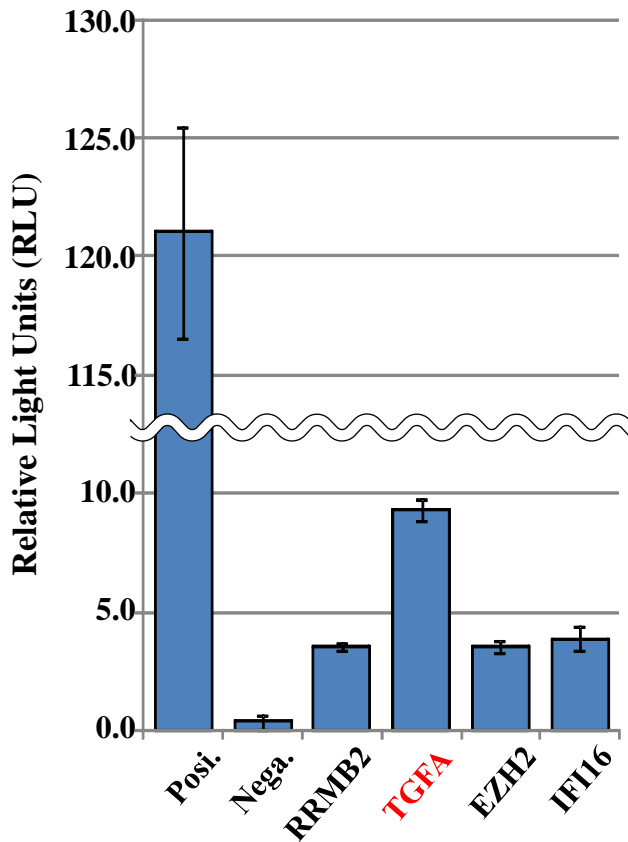
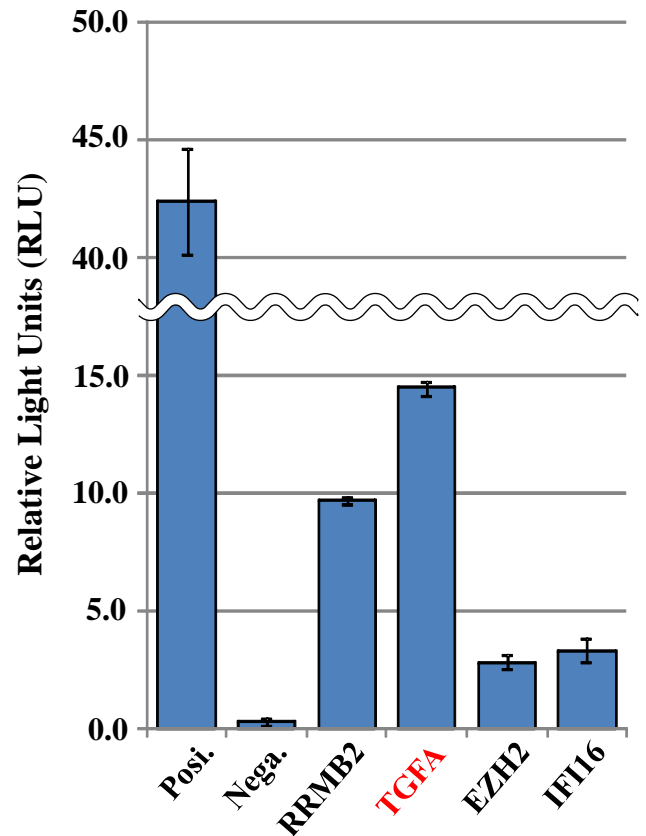


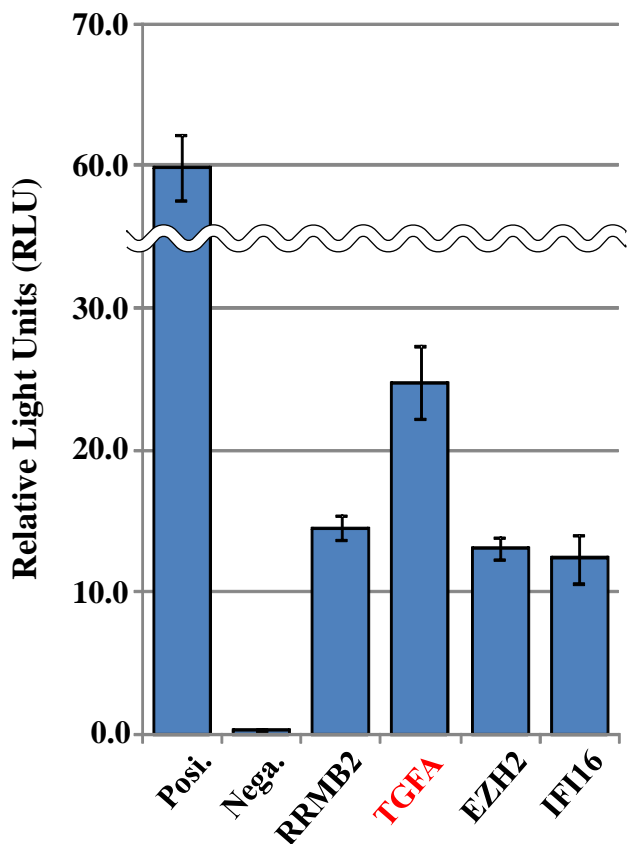
## HeLa cells



## HepG2 cells



## Hep3B cells



Posi.: pGL3 Control Vector  
(SV40 promoter)

Nega.: Empty Vector

RRMB2: pGL4-phRRMB2 (RDB# 7346)

**TGFA**: pGL4-phTGFA (**RDB# 7348**)

EZH2: pGL4-phEZH2 (RDB# 7370)

IFI16: pGL4-phIFI16 (RDB#7372)

[ GENETYX : Nucleotide Sequence Homology Data ]

Date : 2010.03.02

1st Nucleotide Sequence

File Name : Reference Seq.gnu  
Sequence Size : 5547

2nd Nucleotide Sequence

File Name : RDB7348F.fasta  
Sequence Size : 658

Unit Size to Compare = 1  
Pick up Location = 1

[99.531% / 639 bp] INT/OPT. Score : < 1456/ 2518 >

```
1'          GG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCG-AGGAT
          ** *****
1'' GTGCCAGAAC ATTTCTCTGG CCTAACTGGC CGGTACCTGA GCTCGCTAGC CTCGAAGGAT

42' TGATTTACAC TGGTGCTTCC TGCCCAAATG TTGAGACCAA TGGCCTGGTG CTTCCTTCT
          *****
61'' TGATTTACAC TGGTGCTTCC TGCCCAAATG TTGAGACCAA TGGCCTGGTG CTTCCTTCT

102' GAAACTAGGT TGCTCTACTT ACATGAAACA AACTGGGCAG AGGTCAACCG TGAGAGCCTG
          *****
121'' GAAACTAGGT TGCTCTACTT ACATGAAACA AACTGGGCAG AGGTCAACCG TGAGAGCCTG

162' AGCCTCCCCA AGTAAACAGC AAAAGATTCC CCAGGCCCAA CAGCCCCCAC CCCACCTTC
          *****
181'' AGCCTCCCCA AGTAAACAGC AAAAGATTCC CCAGGCCCAA CAGCCCCCAC CCCACCTTC

222' AAGGAAAGTG GATCTACCCG GAGCACGTAG GCCAGAGGAG GCAGGAGAAG AGGGTCAGTC
          *****
241'' AAGGAAAGTG GATCTACCCG GAGCACGTAG GCCAGAGGAG GCAGGAGAAG AGGGTCAGTC
```



```

282' CGTGAGCTCC GGTACCTGG AGAACATGAA TCTCCGGGT GACTGTCCC CATGAGGGTC
*****
301" CGTGAGCTCC GGTACCTGG AGAACATGAA TCTCCGGGT GACTGTCCC CATGAGGGTC

342' ACCGAGGAAC CTATGGATCT TCCACTCTTC GCCCAGAATG TCTTCCCTCT ATC-CCCTCC
*****
361" ACCGAGGAAC CTATGGATCT TCCACTCTTC GCCCAGAATG TCTTCCCTCT ATCTCCCTCC

401' ACCTCCCAA ATTCCAGCAC CAGGGGCCAC CTCAGAGCCA CAAATCCTGA AAGGACCACC
*****
421" ACCTCCCAA ATTCCAGCAC CAGGGGCCAC CTCAGAGCCA CAAATCCTGA AAGGACCACC

461' CAGGTGACTC GGGCCACAC ACCCCTCTTT CGGGGTACAC TTGGTGGCAG GCTAGCAGGC
*****
481" CAGGTGACTC GGGCCACAC ACCCCTCTTT CGGGGTACAC TTGGTGGCAG GCTAGCAGGC

521' TTTTGGCCTC AGCTGGTGGT GCCATATAAC CAGATTCGTC ACAGAGACCC ATTTTTTATC
*****
541" TTTTGGCCTC AGCTGGTGGT GCCATATAAC CAGATTCGTC ACAGAGACCC ATTTTTTATC

581' AGTCCCAGGC CAGAAGTACG AAGACTGATC TTAACGATGT GGCCTGCCTG GGAGGTAAGG
***** **
601" AGTCCAAGC CAGAAGTACG AAGACTGATC TTAACGATGT GGCCTGCCTG GGAGGTAG

```

1st Nucleotide Sequence

File Name : Reference Seq. gnu  
Sequence Size : 5547

2nd Nucleotide Sequence

File Name : RDB7348R. fasta (Complementary)  
Sequence Size : 695

Unit Size to Compare = 1  
Pick up Location = 1



[93.642% / 692 bp] INT/OPT. Score : < 1118/ 2403 >

721' ACCACTTTCC TTGAGCCAAG TCTTGGCAAG CGGCCGGCGA AACTCACAGG TCCCTTTCCT  
\*\*\*\*\* \* \* \* \* \* \* \* \* \*

1" CCGGGCAAA AACTTCACCA AGGTCCCCTT TTTCNTGGGT

781' GGCTGCGTCC CCAGCC--TC CAGCC--TTCC CC--GCCCA GAGATG--CCC CA--GGAGCGG  
\* \* \*\* \* \*\*\* \* \*\*\*\*\* \*\* \* \*\*\*\*\* \*\*\*\*\* \*\* \* \*\*\*\*\*

40" TGGGGTCCCC CAGGCCTTCC CAGCCTTTCC CCGGCCCCCA GAGATGCCCC CAGGGAGCGG

834' CCCCTC--GGT GTAGGTAACG GGTGCCC--GG GCGGCTCCGC TCCGCCGCCT AGAGCC--TGG  
\*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*

100" CCCCTCGGGT GTAGGTAACG GGTGCCC GGG GCGGCTCCGC TCCGCCGCCT AGAGCCTTGG

891' AAGCCGCCAC -TGGGCCCA GGACAATCCG GCTACGCGGC CGGCGCCGAC CCCGCACGCT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

160" AAGCCGCCAC TTGGGCCCA GGACAATCCG GCTACGCGGC CGGCGCCGAC CCCGCACGCT

950' GGAGTCCGCT GCCGCACGGC GCTGGCAGTC GGGGGTGGTG TCTGAAGTCA GGCCTTCCT  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

220" GGAGTCCGCT GCCGCACGGC GCTGGCAGTC GGGGGTGGTG TCTGAAGTCA GGCCTTCCT

1010' GCCTTTTCGT CGGCCGGGT GCCCGGCTCG CGCCGCCAGG CTCTGGGATC CCAGGTCGCC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

280" GCCTTTTCGT CGGCCGGGT GCCCGGCTCG CGCCGCCAGG CTCTGGGATC CCAGGTCGCC

1070' CCGCCAGCA GCCCGGCC TGCTCGGTGC GCTCAGCGTC CCCGCCCTT ACCCAAACC  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

340" CCGCCAGCA GCCCGGCC TGCTCGGTGC GCTCAGCGTC CCCGCCCTT ACCCAAACC

1130' CCCACCCTCT GTGCCCTCAG GGGGACACC CCATCGGGC GGA--GGGG GGGTCAGCTG  
\*\*\*\*\* \*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

400" CCCACCCTCT GTGCCCTCAG GGGGACACC CCATCGGGC GGGAGGGGG GGGTCAGCTG

1189' TGCCCCGGTC GCCGAGTGGC GAGGAGGTGA CGGTAGCCGC CTTCTATTT CCGCCGGCG  
\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*

460" TGCCCCGGTC GCCGAGTGGC GAGGAGGTGA CGGTAGCCGC CTTCTATTT CCGCCGGCG



1249' GGCAGCGCTG CGGGGCGAGT GCCAGCAGAG AGGCGCTCGG TCCTCCCTCC GCCCTCCCGC  
\*\*\*\*\*  
520" GGCAGCGCTG CGGGGCGAGT GCCAGCAGAG AGGCGCTCGG TCCTCCCTCC GCCCTCCCGC

1309' GCCGGGGGCA GGCCCTGCCT AGTCTGCGTC TTTTCCCAT CAAGATCTGG CCTCGGCGGC  
\*\*\*\*\*  
580" GCCGGGGGCA GGCCCTGCCT AGTCTGCGTC TTTTCCCAT CAAGATCTGG CCTCGGCGGC

1369' CAAGCTTGGC AATCCGGTAC TGTGGTAAA GCCACCATGG AAGATGCCAA AACATTAAG  
\*\*\*\*\*  
640" CAAGCTTGGC AATCCGGTAC TGTGGTAAA GCCACCATGG AAGATGCCAA AACAT